



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

NOV 05 2004

In re Application of

Examiner: Slobodyansky, E.

MARCIREAU ET AL

Art Unit: 1652

Serial No.: **09/744,125**

Filed: September 17, 2001

Title: **MEKKI-INTERACTING FHA PROTEIN**

hereby certify that this correspondence is being transmitted via facsimile to the Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, care of Art Unit 1652, at 703-305-3014 on

Date of Deposit

10/08/2004
J. Marcireau, Sr.
Printed Name of Person Signing Certificate

Signature

DECLARATION UNDER 37 CFR § 1.131 OF PRIOR INVENTION IN A WORLD TRADE ORGANIZATION (WTO) MEMBER COUNTRY

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313

Dear Sir:

Christophe Marcireau declares as follows:

1. I am an inventor of the inventions claimed in U.S. Patent Application Serial No. 09/744,125 filed on September 17, 2001 ("the '125 application").
2. Prior to September 10, 1997 I obtained the nucleic acid of SEQ ID NO:1 in France, a WTO member country.
3. Prior to September 10, 1997, I translated SEQ ID NO:1 and obtained the amino acid sequence of SEQ ID NO:2 in France, a WTO member country.
4. Attached hereto is a machine-generated graph that shows the results of the sequencing of the nucleic acid of SEQ ID NO:1. The sequencing of SEQ ID

NO:1 and its translation to obtain the amino acid sequence of SEQ ID NO:2 was performed under my direction. The machine-generated date on the graph has been redacted, but that date is prior to September 10, 1997. The sequencing was conducted in France, a WTO member country.

5. I declare that all of the foregoing statements are true, recognizing that willful false statements are punishable by fine or imprisonment, or both, under 18 U.S.C. § 1001, and that any such willful false statements may jeopardize the validity of the application or any patent that issues from it.

Date: October the 12th



Christophe Marcireau

mbp3nt [1 to 1257] -> 1-phase Translation

DNA sequence 1603 b.p. GTGGATCCCCCG ... TCGCCCTATAGT linear

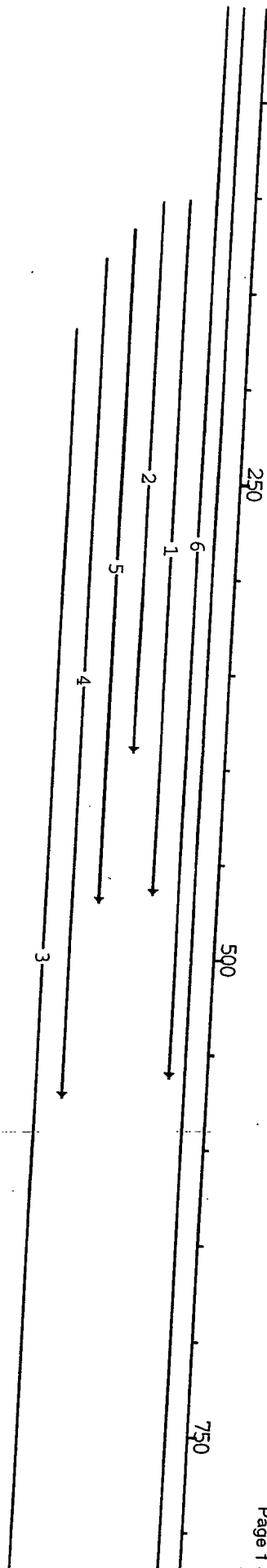
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121/41                               151/51
CCA CCC AGC CCA GCC CCA GCC CCT GGA CTC ACC AAG CGT GTG AAG AAG AGT AAA CAG CCA
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181/61                               211/71
CTT CAG GTG ACC AAG GAT CTG GGC CGC TGG AAG CCT GCA AAT GAC CTC CTG CTC ATA AAT
L Q V T K D L G R W K P A N D L L L I N
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961/321                               991/331
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1201/401                               1231/411
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Ass EST



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 Last assembled: [REDACTED] 16:09:55

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Total in assemblages:	6	2576	100.0%
Total unassembled:	0	0	0.0%
Total dye primer:	0	0	0.0%
Total dye terminator:	0	0	0.0%
Non-373 sequences:	6	2666	103.5%

	Sequences	Bases	Score	Ambiguities
w26888.Assemblage.1	6	831	1773.0	34

w26888.Assemblage.1 Sequences: 6 Bases: 831 Score: 1773.0
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 Sequence Lengths Average: 429 High: 640 Low: 282

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f12127		-> 2	104	392	282	12/03/97	
w00383		-> 5	119	472	347	12/03/97	
t66207		-> 4	135	575	420	12/03/97	
r52839		-> 3	172	831	640	12/03/97	

Unassembled Sequences Sequences: 0 Bases: 0
 File Sample ID Begin End Length Date Chemistry

SMPS HS
untitled 2

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-> G G N N N N T A C C C A G G A C G G A C C C T C C A G A G A C A G G T C C A C G G A G C G C A T C A G G T A C C G C A C G G A A G C C G G E T T T T G
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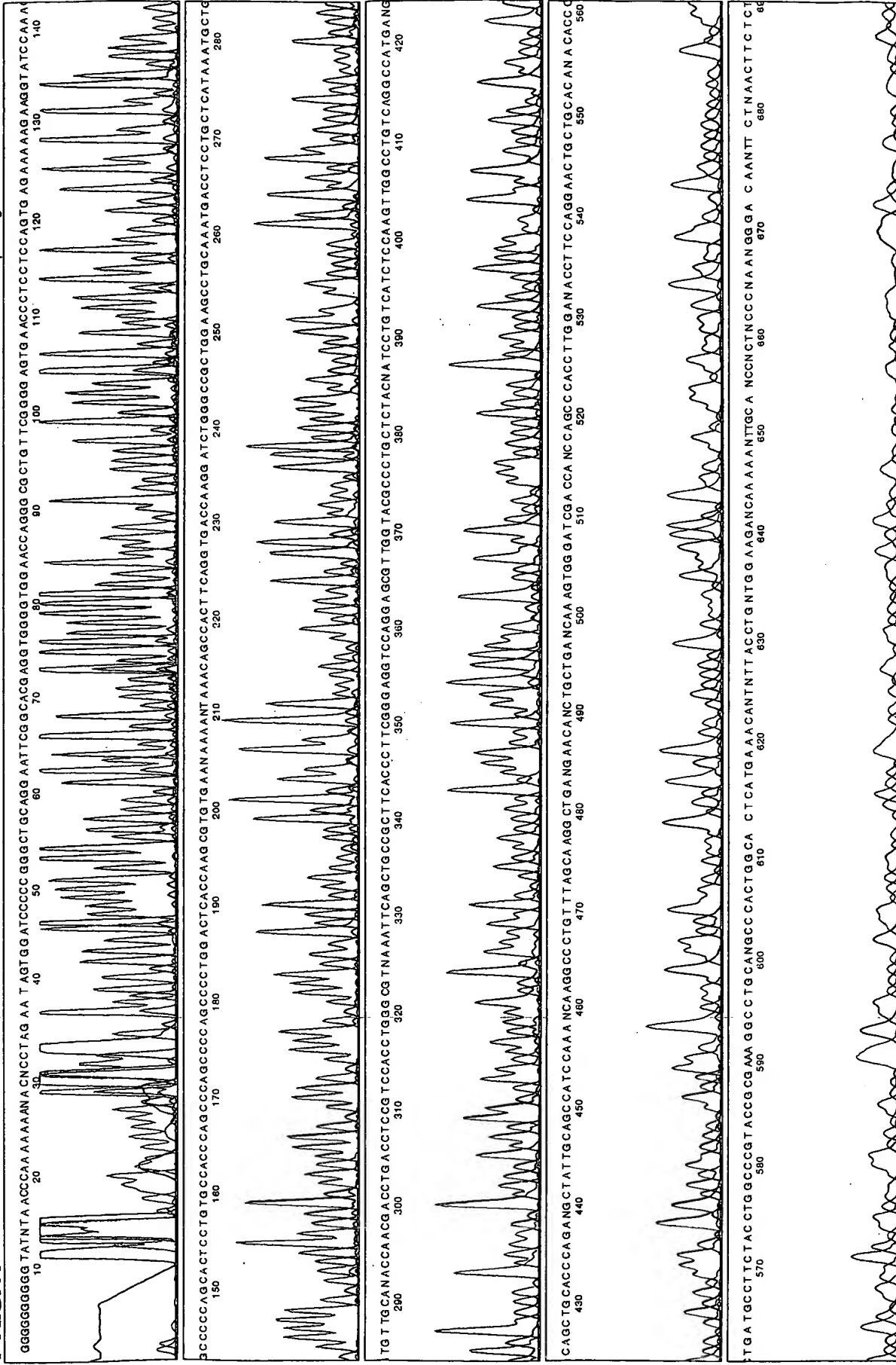
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125 150 175 200 225
-> G C C C T G C G C T G C T A C C G T G C C C G G A G A A A T T G T T G G A T C T G N A G T C T A G A A T G A A T C C T C T A G C C T T T A A G C T A C C T G G T C A G A A T C C T T G G A T G A C C C T G T G G A C C G T
-> G C C - T G C G C T G C T A C C G T G C C C G G A G A A A T T G T T G G A T C T G G C A G T C T A G A A T G A A T C C T C T A G C C T T T A A G C T A C C T G G T C A G A A T C C T T G G A T G A C C C T G T G G A C C G T T
-> G C C C T G C G C T G C T A C C G T G C N G N G G A G A A A T T G T T G G A T C T G G C A G T C T A G A A T G A A T C C T C T A G C N T T T A A G C T A C C T G G T C A G A A T C C T T G G A T G A C C C T G T G G A C C G T T
-> G C C - T G C G C T G C T A C C G T G C C C G G A G A A A T T G T T G G A N C T G G C A G T C T A G A A T G A A T C C T C T C A G C C T T T A A G C T A C C T G G T C A G A A T C C T T G G A T G A C C C T G T G G A C C G T T
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-> C C T C C T A G C C C G T G G T T T G G A A C C A G T G G C T T T G G G A C T G T A A G A G G A T G G A C A A A G A T T C T C A G G G C T G C T A G A T T C A T C C C T G A T G G C A T C A G G C A C T - G C C A G C C G - C T C A - G A G
-> C C T C C T A G C C C T G T G G T T T G G A A C C A G T G G C T T T G G G A C T G T A A G A G G A T G G A C A A A G A T T C T C A G G G C T G C T A G A T T C A T C C C T G A T G G C A T C A G G C A C T - G C - A G C C G - C T C A - G A G
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mbp3nt [1 to 1257] -> 1-phase Translation

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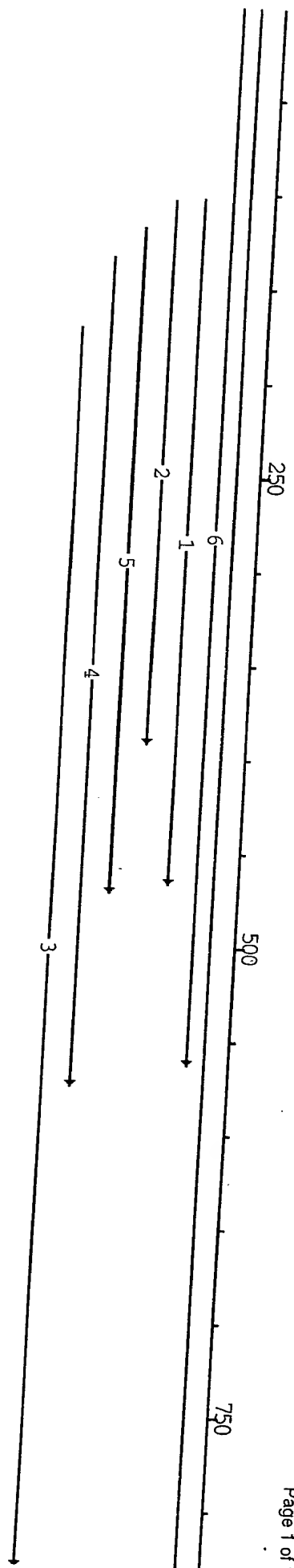
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V D P P G C R N S A R G G V E P G R C S
61/21                               91/31
GGG AGT GAA CCC TCC TCC AGT GAG AAA AAG AAG GTA TCC AAA GCC CCC AGC ACT CCT GTG
G S E P S S S E K K K V S K A P S T P V
121/41                               151/51
CCA CCC AGC CCA GCC CCA GCC CCT GGA CTC ACC AAG CGT GTG AAg AAg AGT AAA CAG CCA
P P S P A P A P G L T K R V K K S K Q P
181/61                               211/71
CTT CAG GTG ACC AAG GAT CTG GGC CGC TGG AAg CCT GCA AAT GAC CTC CTG CTC ATA AAT
L Q V T K D L G R W K P A N D L L L I N
241/81                               271/91
GCT GTG TTG CAg ACC AAC GAC CTG ACC TCC GTC CAC CTG GGC GTG AAA TTC AGC TGC CGC
A V L Q T N D L T S V H L G V K F S C R
301/101                               331/111
TTC ACC CTT CGG GAG GTC CAG GAG CGT TGG TAC GCC CTG CTC TAC gAT CCT GTC ATC TCC
F T L R E V Q E R W Y A L L Y D P V I S
361/121                               391/131
AAG TTG GCC TGT CAG GCC ATG AGG CAG CTG CAC CCA GAG GCT ATT GCA GCC ATC CAG AGC
K L A C Q A M R Q L H P E A I A A I Q S
421/141                               451/151
AAG GCC CTG TTT AGC AAG GCT GAG GAG CAG CTG CTG AGC AAA GTG GGA TCG ACC AGC CAG
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481/161                               511/171
CCC ACC TTG GAG ACC TTC CAG GAC CTG CTG CAC AGA CAC CCT GAT GCC TTC TAC CTG GCC
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541/181                               571/191
CGT ACC GCG AAG GCC CTG CAG GCC CAC TGG CAG CTC ATG AAG CAG TAT TAC CTG CTG GAG
R T A K A L Q A H W Q L M K Q Y Y L L E
601/201                               631/211
GAC CAG ACA GTG CAG CCG CTG CCC AAA GGG GAC CAA GTG CTG AAC TTC TCT GAT GCA GAG
D Q T V Q P L P K G D Q V L N F S D A E
661/221                               691/231
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M V A D R R Q K R E I R Q L E Q E L H K
781/261                               811/271
TGG CAG GTG CTA GTG GAC AGC ATC ACA GGC ATG AGC TCT CCG GAC TTC GAC AAC CAg ACA
W Q V L V D S I T G M S S P D F D N Q T
841/281                               871/291
CTG GCA GTG CTG CGG GGC CGC ATG GTG CGG TAC CTG ATG CGC TCG CGT GAG ATC ACC CTG
L A V L R G R M V R Y L M R S R E I T L
901/301                               931/311
GGC AGA GCA ACC AAG GAT AAC CAG ATT GAT GTG GAC CTG TCT CTG GAG GGT CCG GCC TGG
G R A T K D N Q I D V D L S L E G P A W
961/321                               991/331
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K I S R K Q G V I K L K N N G D F F I A
1021/341                               1051/351
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N E G R R P I Y I D G R P V L C G S K W
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1141/381                               1171/391
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Q D L I A L I R A E L P R S H H S E E W
1201/401                               1231/411
TGG CAG GAC TCG TGG GCC CTC TCC GGC CTG TTT CCC CTG CCA CTC CAG CCC CCT TGA
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Ass EST



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 Last assembled: 16:09:55

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Total in assemblages:	6	2576	100.0%
Total unassembled:	0	0	0.0%
Total dye primer:	0	0	0.0%
Total dye terminator:	0	0	0.0%
Non-373 sequences:	6	2666	103.5%

	Sequences	Bases	Score	Ambiguities
w26888.Assemblage.1	6	831	1773.0	34

	Sequences:	6	Bases:	831	Score:	1773.0
w26888.Assemblage.1	Average:	3.2	High:	6	Low:	1
Redundancy	Average:	429	High:	640	Low:	282
Sequence Lengths						

File	Sample	ID	Begin	End	Length	Date	Chemistry
w26888		-> 6	0	562	535	12/03/97	
aa134651		-> 1	103	467	352	12/03/97	
f12127		-> 2	104	392	282	12/03/97	
w00383		-> 5	119	472	347	12/03/97	
t66207		-> 4	135	575	420	12/03/97	
r52839		-> 3	172	831	640	12/03/97	

Unassembled Sequences	Sequences:	0	Bases:	0		
File	ID	Begin	End	Length	Date	Chemistry

SI MBPS HS



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f12127 -> C C G A A G C G N N C T T T T T G
w00383 -> G

w26888 .Assemblage.1 G C C C T G C G G C T G C T A C C G T C G C G C G G A G A A A T T G T T G G A T C T G G C A G T C T G G A A T G A A T C T C C T C T C A G C C T T T A A G C T C A C C T G G T C A G A A T C C T T G G A T G A G C C T G T G G A C C G T T
125 150 175 200 225
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f12127 -> G C C C T G C G G C T G C T A C C G T C G N C G N G G A G A A A T T G T T G G N C T G G C A G T C T A G G A A T G A A T C C T C T C A G C N T T T A A G C T C A C C T G G T C A G A A T C C T T G G A T G A G C C T G T G G A C C G T T
w00383 -> G C C - T G C G G C T G C T A C C G T C G C G C G G A G A A A T T G T T G G A N C T G G C A G T C T A G G A A T G A A T C C T C T C A G C C T T T A A G C T C A C C T G G T C A G A A T C C T T G G A T G A G C C T G T G G A C C G T T
t66207 -> C C G T C G C C - C G G A G A A T T G T T G G A T C T G G C A G T C T A G G A A T G A A T C C T C T C A G C C T T T A A G C T C A C C T G G T C A G A A T C C T T G G A T G A G C C T G T G G A C C G T T
r52839 -> G G A A T G A A T C C T C T C T C A G C C T T T A A G C T C A C C T G G T C A G A A T C C T T G G A T G A G C C T G T G G A C C C T T

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250 275 300 325 350
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aa134651 -> C C T C C T A G C C C C T G T G T T T G G A A C C A G T G G C T T T G G G A C T G T A A G A G G A T G G A C A A A G A T T C T C A G G G C T G C T A G A T T C A T C C C T G A T G G C A T C A G G C A C T - G C C A G C C G C T C A - G A G
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375 400 425 450 475
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t66207 -> G A T G A G A G T C A C T G C C A G G G C A - G A A - G C - G A - G C C T C C - T C C C A - G G C C T T G G G - A - C C A T C C C - T A A A C - G G A G A A - G C T C C T C C A G G T T - T A T C A A G A G A A G A A G T T C - G A T G A T
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52839
-> GCTTGCAGATTGANCCTCTTNTTATTAAATTGTTGTGTTTGCAGACCAACGACTTAACCTTCNTTCACCTTGGGNTGAAATTTNAGTTTNCCTTTAACCTTTTNGGAAGTTTCAG

Model 377
Version 3.0
ABI100
Version 3.0

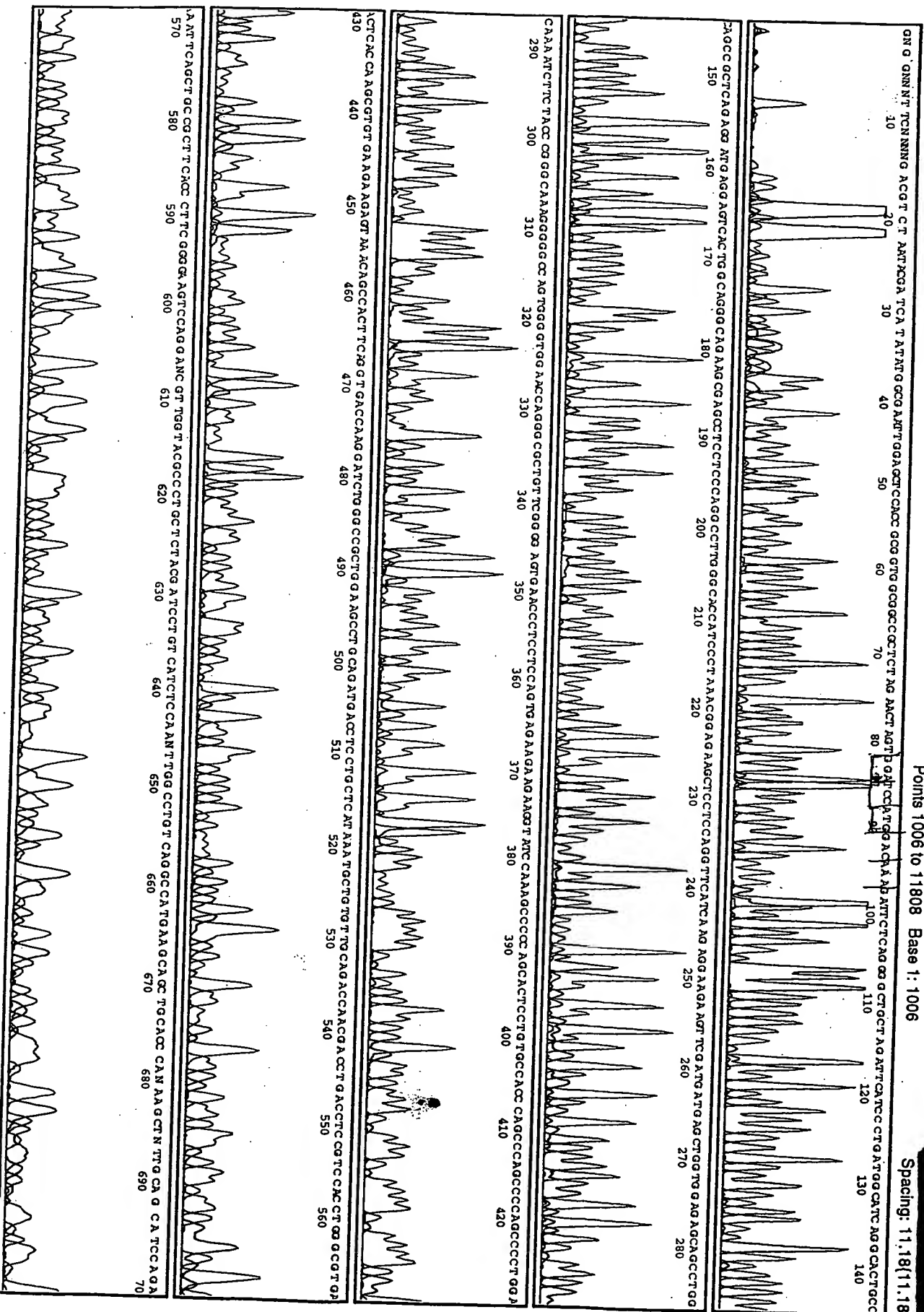
09•CM 13

CM 13
Lane 9

Signal G:104 A:318 T:111 C:113
DT4%Ac(A Set-AnyPrimer)
SN 95080645
Points 1006 to 11808 Base 1: 1

Spacing: 11.18(11.18)

Page 1 of 2



07•CM 21
CM 21

11 - 1000

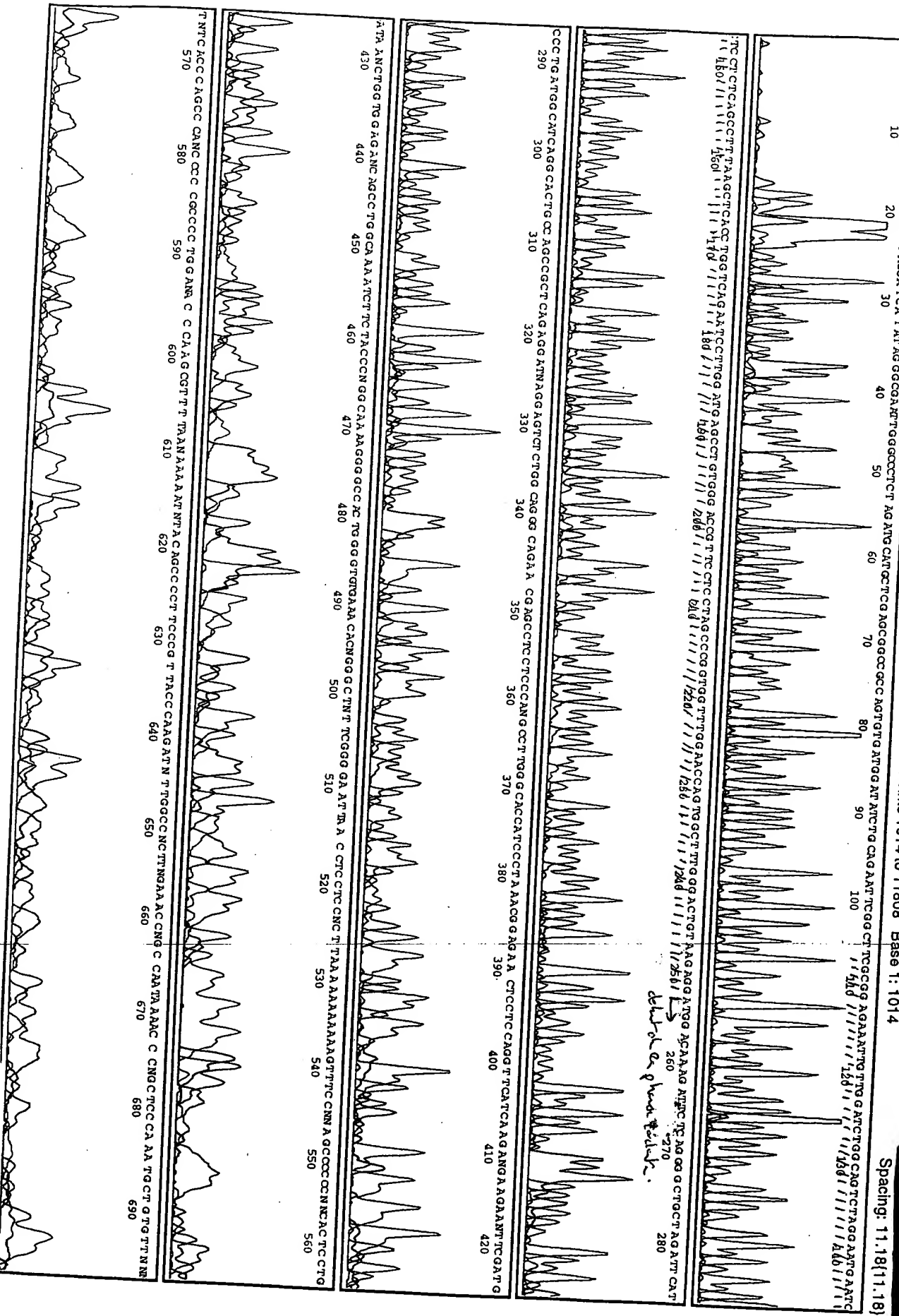
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SN 9508064E

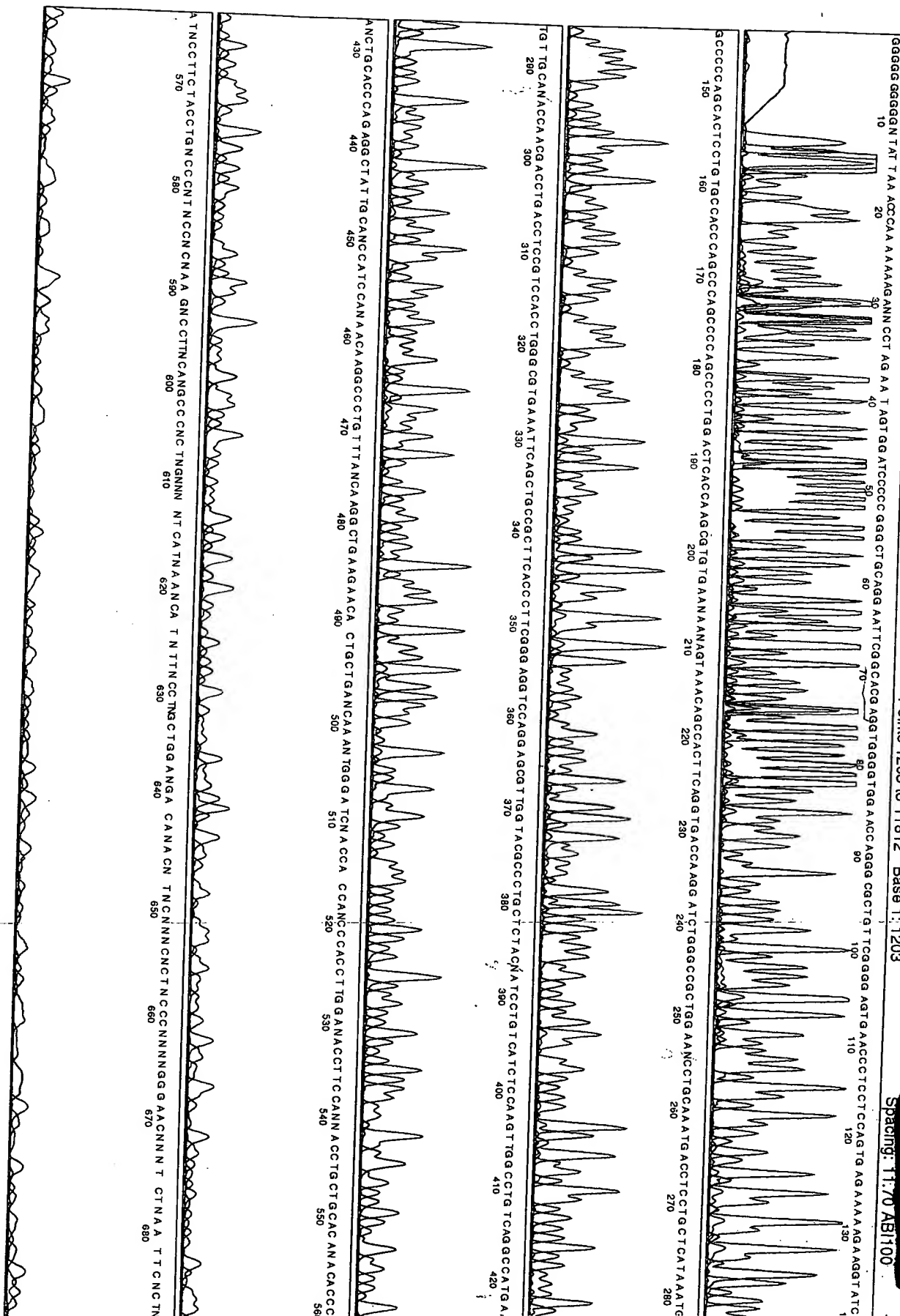
GNNNNNNTNGCNNNGCATNTT

Larrie /
AT AG GG

Points 1014 to 11808 Base 1..1014

Spacing: 11.18(11.18)







Model 377
Version 2.1.1

20•CM 3
CM 3
Lane 20

Signal G:483 A:1087 T:367 C:416
*D14%Ac(A Set:Any/Primer)
S/N 95080645
Points 1209 to 11812 Base 1: 1209

Spacing: 11.29 ABI100

